Listing of claims:

1. **(Withdrawn/Currently amended)** A method for screening substances which are potential inhibitors of ~~transcription~~ expression of bacterial T-box regulated genes, comprising the steps of:

a) incubating one or more assay mixtures to produce a readthrough mRNA product, wherein the assay mixtures comprise ~~comprising~~: a template DNA that comprises: (i) a bacterial promoter, (ii) a *glyQS* leader ~~of a T-box regulated gene~~, including a transcription start site, and (iii) a downstream polynucleotide of sufficient length for detection of a read-through mRNA product; divalent magnesium ~~metal~~ cations at a concentration equal to or higher than 30 mM; nucleoside triphosphates; dinucleotides corresponding to and encoded by the transcription start site of the *glyQS* leader; bacterial RNA polymerase complex; and tRNA specific for a specifier sequence located in the *glyQS* leader; and

b) incubating a potential inhibitor substance with one or more assay mixtures to produce a readthrough mRNA product, wherein the assay mixtures comprise ~~comprising~~: a template DNA that comprises: (i) a bacterial promoter, (ii) a *glyQS* leader ~~of a T-box regulated gene~~, including a transcription start site, and (iii) a downstream polynucleotide of sufficient length for detection of a read-through mRNA product; divalent magnesium ~~metal~~ cations at a concentration of about 30 mM or higher; nucleoside triphosphates; dinucleotides corresponding to and encoded by the transcription start site of the *glyQS* leader; bacterial RNA polymerase complex; and tRNA specific for a specifier sequence located in the *glyQS* leader; ~~and~~

c) comparing the ~~amount of~~ fraction of total mRNA products corresponding to the read-through mRNA product produced in step a) with the ~~amount~~ fraction of total mRNA products corresponding to the read-through mRNA product produced in step b)

wherein a lesser ~~amount~~ fraction of ~~a~~ the read-through mRNA product ~~determined for~~ produced in step b) in comparison with step a) indicates that said potential inhibitor substance inhibits transcriptional readthrough of said ~~T-box~~ *glyQS* leader and therefore is an inhibitor of expression of bacterial T-box regulated genes.

2. **(Withdrawn/Currently amended)** The method recited in claim 1 wherein the divalent ~~metal cation is Mg^{2+}~~ magnesium concentration is about 30 mM.

3. **(Withdrawn)** The method recited in claim 1 wherein the nucleoside triphosphates are selected from the group consisting of adenosine triphosphate, guanosine triphosphate, cytosine triphosphate, and uridine triphosphate, and any combination of one or more of these.

4. **(Withdrawn)** The method recited in claim 1 wherein the dinucleotides are selected from the group consisting of ApA, ApC, ApU, ApG, GpA, GpC, GpU, GpG, CpA, CpC, CpU, CpG, UpA, UpC, UpU, and UpG.

5. **(Withdrawn/Currently amended)** The method recited in claim 1 wherein the bacterial promoter is selected from the group consisting of ~~the~~ a *B. subtilis glyQS* promoter and ~~the~~ a *B. subtilis rpsD* promoter.

6. **(Withdrawn)** The method recited in claim 1 wherein the downstream polynucleotide of sufficient length for detection of a read-through mRNA product comprises a polynucleotide which is from about 30 to 150 nucleotide residues in length.

7. **(Withdrawn/Currently amended)** The method recited in claim 1 wherein the tRNA specific for a specifier sequence located in the *glyQS* leader is *B. subtilis* $tRNA^{Gly}$.

8. **(Withdrawn/Currently amended)** The method recited in claim 1 wherein the RNA polymerase is purified from either *B. subtilis* or *Escherichia coli.*

9. **(Withdrawn/Currently amended)** The method recited in claim 1 wherein the *glyQS* leader comprises a ~~polynucleotide~~ variant *glyQS* leader sequence which is a variant of a wild-type ~~glycine synthetase~~ *glyQS* leader from a Gram positive bacterial strain, wherein the variant *glyQS* leader sequence comprises modifications to one or both ~~of the wild-type~~ *glyQS* leader specifier and ~~wild-type~~ antiterminator sequences as compared to the wild-type *glyQS* leader.

10. **(Withdrawn/Currently amended)** The method recited in claim 1 wherein the tRNA specific for a specifier sequence located in the *glyQS* leader is a variant of a wild-type tRNA ~~wherein any one or more of the~~ in which either or both wild-type anticodon sequence, or ~~the~~

wild-type discriminator sequence, ~~and the transcription start site is~~ are altered to complement ~~with~~ the *glyQS* leader sequence.

11. **(Withdrawn/Currently amended)** The method recited in claim 1 wherein the *glyQS* leader comprises a variant *glyQS* leader ~~polynucleotide~~ sequence which is a variant of a wild-type ~~glycine synthetase~~ *glyQS* leader ~~sequence~~ from a Gram positive bacterial strain, wherein the variant *glyQS* leader sequence comprises modifications to one or both ~~of the~~ wild-type *glyQS* leader specifier and ~~wild-type~~ antiterminator sequences, and wherein the tRNA specific for a specifier sequence located in the ~~wild-type~~ *glyQS* leader is a variant of a wild-type tRNA ~~wherein~~ in which either or both ~~of the~~ wild-type anticodon sequence, ~~and the~~ or wild-type discriminator sequence are altered to complement ~~with~~ the variant *glyQS* leader sequence.

12. **(Withdrawn/Currently amended)** The method recited in claim 1 wherein the assay ~~mixtures are~~ comprises an *in vitro* halted-complex bacterial transcription assay ~~systems~~.

13. **(Withdrawn/Currently amended)** A method for identifying inhibitors of ~~transcription~~ expression of bacterial T-box regulated genes, comprising:

providing two or more *in vitro* halted-complex bacterial transcription assay systems which comprise a template DNA comprising: (i) a bacterial promoter, (ii) a polynucleotide comprising a portion of a leader from ~~the~~ *B. subtilis glyQS* gene and ~~includes~~ including a transcription start site, and (iii) a downstream polynucleotide of sufficient length for detection of a read-through mRNA product; RNA polymerase, and uncharged *B. subtilis* $tRNA^{Gly}$, wherein at least one or more of said assay systems comprises a test substance, and wherein at least one or more of said assay systems lacks a test substance, and comparing the ~~amount of~~ fraction of total mRNA products corresponding to *B. subtilis glyQS* read-through mRNA produced in each of said assay systems, wherein a test substance is considered an inhibitor if it effects a lesser ~~amount of~~ fraction of total mRNA products corresponding to the *B. subtilis glyQS* read-through mRNA produced in an assay system comprising ~~such~~ said test substance as compared to an assay system lacking ~~any~~ said test substance.

14. **(Withdrawn/Currently amended)** The method recited in claim 13 wherein the bacterial promoter is selected from the group consisting of ~~the~~ a *B. subtilis glyQS* promoter and ~~the~~ a *B. subtilis rpsD* promoter.

15. **(Withdrawn/Currently amended)** The method recited in claim 13 wherein the RNA polymerase is purified from either *B. subtilis* or *Escherichia coli.*

16. **(Withdrawn/Currently amended)** The method recited in claim 13 wherein ~~the sequence of~~ the polynucleotide comprising a portion of the leader from the *B. subtilis glyQS* ~~leader~~ gene ~~is~~ comprises a variant ~~of the wild-type~~ *B. subtilis glyQS* leader sequence~~, wherein the variant comprises~~ comprising modifications to one or both ~~of the wild-type~~ *B. subtilis glyQS* leader specifier and ~~wild-type~~ antiterminator sequences as compared to the wild-type *glyQS* leader, and

wherein the uncharged *B. subtilis* $tRNA^{Gly}$ is a variant of a wild-type *B. subtilis* $tRNA^{Gly}$ in which either or both wild-type anticodon sequence and wild-type discriminator sequence are altered to complement the variant *B. subtilis glyQS* leader sequence.

17. **(Cancelled)**

18. **(Currently amended)** ~~An~~ A purified *in vitro* assay system for screening substances which are potential inhibitors of ~~transcription~~ expression of bacterial T-box regulated genes, comprising:

a) one or more assay mixtures comprising: a template DNA that comprises: (i) a bacterial promoter, (ii) a *glyQS* leader ~~of a T-box regulated gene~~, including a transcription start site, and (iii) a downstream polynucleotide of sufficient length for detection of a read-through mRNA product; divalent magnesium ~~metal~~ cations at a concentration of about 30 mM or higher; nucleoside triphosphates; dinucleotides corresponding to and encoded by the transcription start site of the *glyQS* leader; bacterial RNA polymerase complex; and tRNA specific for a specifier sequence located in the *glyQS* leader; and

b) one or more assay mixtures comprising: a potential inhibitor substance; a template DNA that comprises: (i) a bacterial promoter, (ii) a *glyQS* leader ~~of a T-box regulated gene~~,

including a transcription start site, and (iii) a downstream polynucleotide of sufficient length for detection of a read-through mRNA product; divalent magnesium ~~metal~~ cations at a concentration of about 3 mM or higher; nucleoside triphosphates; dinucleotides corresponding to and encoded by the transcription start site of the *glyQS* leader; bacterial RNA polymerase complex; and tRNA specific for a specifier sequence located in the *glyQS* leader.

19. **(Currently amended)** The assay system recited in claim 18 wherein the divalent ~~metal cation is~~ magnesium cation concentration is about 30 mM.

20. **(Original)** The assay system recited in claim 18 wherein the nucleoside triphosphates are selected from the group consisting of adenosine triphosphate, guanosine triphosphate, cytosine triphosphate, and uridine triphosphate, and any combination of one or more of these.

21. **(Original)** The assay system recited in claim 18 wherein the dinucleotides are selected from the group consisting of ApA, ApC, ApU, ApG, GpA, GpC, GpU, GpG, CpA, CpC, CpU, CpG, UpA, UpC, UpU, and UpG.

22. **(Currently amended)** The assay system recited in claim 18 wherein the bacterial promoter is selected from the group consisting of ~~the~~ a *B. subtilis glyQS* promoter and ~~the~~ a *B. subtilis rpsD* promoter.

23. **(Original)** The assay system recited in claim 18 wherein the downstream polynucleotide of sufficient length for detection of a read-through mRNA product comprises a polynucleotide which is from about 30 to 150 nucleotide residues in length.

24. **(Currently amended)** The assay system recited in claim 18 wherein the tRNA specific for a specifier sequence located in the *glyQS* leader is *B. subtilis* $tRNA^{Gly}$.

25. **(Currently amended)** The assay system recited in claim 18 wherein the RNA polymerase is purified from either *B. subtilis* or *Escherichia coli.*

26. **(Currently amended)** The assay system recited in claim 18 wherein the *glyQS* leader comprises a ~~polynucleotide~~ variant *glyQS* leader sequence which is a variant of a wild-type ~~glycine synthetase~~ *glyQS* leader from a Gram positive bacterial strain, wherein the variant *glyQS*

leader sequence comprises modifications to one or both ~~of the wild-type~~ *glyQS* leader specifier and ~~wild-type~~ antiterminator sequences as compared to the wild-type *glyQS* leader.

27. **(Currently amended)** The assay system recited in claim 18 wherein the tRNA specific for a specifier located in the *glyQS* leader is a variant of a wild-type tRNA ~~wherein any one or more of the~~ in which either or both wild-type anticodon sequence, or ~~the~~ wild-type discriminator sequence, ~~and the transcription start site~~ ~~is~~ are altered to complement ~~with~~ the *glyQS* leader sequence.

28. **(Currently amended)** The assay system recited in claim 18 wherein the leader comprises a ~~polynucleotide~~ variant *glyQS* leader sequence which is a variant of a wild-type ~~glycine synthetase~~ *glyQS* leader ~~sequence~~ from a Gram positive bacterial strain, wherein the variant *glyQS* leader sequence comprises modifications to one or both ~~of the wild-type~~ *glyQS* leader specifier~~, and wild-type~~ antiterminator sequences as compared to the wild-type *glyQS* leader, and wherein the tRNA specific for a specifier sequence located in the ~~wild-type~~ *glyQS* leader is a variant of a wild-type tRNA ~~wherein~~ in which either or both ~~of the~~ wild-type anticodon sequence, or ~~and the~~ wild-type discriminator sequence are altered to complement ~~with~~ the variant *glyQS* leader sequence.

29. **(Currently amended)** The assay system recited in claim 18 wherein the assay ~~mixtures are~~ comprises an *in vitro* halted-complex bacterial transcription assay ~~systems~~.

30. **(Currently amended)** ~~An~~ A purified *in vitro* assay ~~system~~ for identifying inhibitors of ~~transcription~~ expression of bacterial T-box regulated genes, comprising:

two or more *in vitro* halted-complex bacterial transcription assay systems which comprise a template DNA comprising: (i) a bacterial promoter, (ii) a polynucleotide comprising a portion of a leader from ~~the~~ *B. subtilis* ~~glyQS~~ *glyQS* gene, including a transcription start site, and (iii) a downstream polynucleotide of sufficient length for detection of a read-through mRNA product; RNA polymerase, and uncharged *B.* ~~subtilis~~ *subtilis* $tRNA^{Gly}$, wherein at least one or more of said assay systems comprises a test substance, and wherein at least one or more of said assay systems lacks a test substance.

31. **(Currently amended)** The assay ~~system~~ recited in claim 30 wherein the bacterial promoter is selected from the group consisting of ~~the~~ a *B. subtilis glyQS* promoter and ~~the~~ a *B. subtilis rpsD* promoter.

32. **(Currently amended)** The assay ~~system~~ recited in claim 30 wherein the RNA polymerase is purified from either *B. subtilis* or *Escherichia coli.*

33. **(Currently amended)** The assay ~~system~~ recited in claim 30 wherein ~~the sequence of~~ the polynucleotide comprising a portion of the leader from the *B. subtilis glyQS* ~~leader~~ gene ~~is~~ comprises a variant ~~of the wild-type~~ *B. subtilis glyQS* leader sequence~~, wherein the variant comprises~~ comprising modifications to one or both ~~of the wild-type~~ *B. subtilis glyQS* leader specifier and ~~wild-type~~ antiterminator sequences as compared to the wild-type *glyQS* leader, and

wherein the uncharged *B. subtilis* $tRNA^{Gly}$ is a variant of a wild-type *B. subtilis* $tRNA^{Gly}$ in which either or both wild-type anticodon sequence and wild-type discriminator sequence are altered to complement the variant *B. subtilis glyQS* leader sequence.

34. **(Cancelled)**

35. **(Cancelled)**